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(54) Title: METHOD AND MATERIALS FOR POLYAMINE CATALYZED BISULFITE CONVERSION OF CYTOSINE TO URACIL

(57) Abstract: The invention provides methods and materials for conversion of cytosine to uracil. In some embodiments, a nucleic acid, such as gDNA, is reacted with bisulfite and a polyamine catalyst, such as a triamine or tetra-amine. Optionally, the bisulfite comprises magnesium bisulfite. In other embodiments, a nucleic acid is reacted with magnesium bisulfite, optionally in the presence of a polyamine catalyst and/or a quaternary amine catalyst. Also provided are kits that can be used to carry out methods of the invention.



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METHOD AND MATERIALS FOR POLYAMINE CATALYZED BISULFITE CONVERSION OF CYTOSINE TO URACIL

[0001] This application claims benefit of priority to US Provisional Application Serial Nos. 60/499,113 filed August 29, 2003 and 60/620,942 filed November 17, 2003, each of which is hereby incorporated by reference.

FIELD

[0002] The invention relates generally to methods and materials for the specific conversion of cytosine to uracil.

BACKGROUND

[0003] Assessment of methylation of DNA is useful in many research, diagnostic, medical, forensic, and industrial fields. Particularly, methylation of cytosine in genomic DNA has been correlated with lack of gene expression, and in some instances can be indicative of early and frequent alterations found in some cancers. Thus, the ability to assess the methylation status of DNA is significant.

[0004] Key to this assessment is converting cytosine to uracil. One basic method for such conversion, employing sodium bisulfite, is well known. Over the years, the method has been improved in attempts to overcome disadvantages that include tedious procedures, lengthy reaction times, and DNA degradation. The most commonly used protocol is taught by J. Herman, *Proc. Natl. Acad. Sci.* **93**, 9821-26 (1996), incorporated herein by reference in its entirety. This method involves denaturation, reaction with sodium bisulfite in the presence of hydroquinone, and subsequent completion of the modification by treatment with NaOH. Despite the attempts to improve the protocol, current procedures require to pre-denaturation of the genomic DNA (gDNA) to single stranded DNA (ssDNA), preparation fresh solutions of sodium bisulfite (NaHSO₃), typically about 3M, and inclusion of an

antioxidant (e.g., hydroquinone). The protocol also involves long reaction times and tedious clean-up procedures.

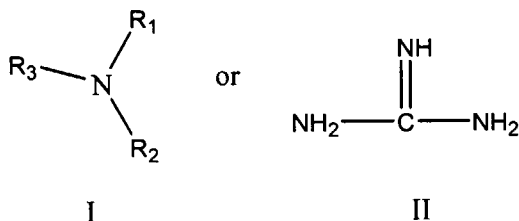
[0005] In addition, the currently employed sodium bisulfite protocols are plagued by reports of incomplete conversion, irreproducible results, and other problems. In some cases, the reaction can result in significant DNA degradation (reportedly as high as 96%), making it difficult to obtain enough sample for further analysis. See. S.J. Clark et al. *Nucleic Acid Research* 2001, **29** no. 13, e65. Given the importance of assessment of DNA methylation, it can be seen that there is a need for improved methodologies for conversion of cytosine to uracil.

[0006] It has been discovered that bisulfite methods that employ magnesium bisulfite, polyamine compounds, and/or quaternary amine compounds provide useful alternatives to sodium bisulfite conversion reactions. These discoveries are the subjects of co-owned applications entitled "Method And Materials For Polyamine Catalyzed Bisulfite Conversion Of Cytosine To Uracil" (U.S. application Ser. No. 60/499,113 filed August 29, 2003, and also application Ser. No. 60/520,942 having the same title and filed November 17, 2003), "Method And Materials For Quaternary Amine Catalyzed Bisulfite Conversion Of Cytosine To Uracil" (U.S. application Ser. No. 60/499,106 filed August 29, 2003, and also application Ser. No. 60/523,054 having the same title and filed November 17, 2003), and "Method and Materials for Bisulfite Conversion of Cytosine to Uracil (U.S. application Ser. No. 60/499,082 filed August 29, 2003, and also application Ser. No. 60/523,056 having the same title and filed November 17, 2003), all of which are hereby incorporated by reference in their entirety. Improved methods for purifying the bisulfite-treated sample have also been discovered. These discoveries are the subject of co-owned applications entitled: "Improved Bisulfite Method" (U.S. application Ser. No. 60/498,996 filed August 29, 2003, and also application Ser. No. 60/520,941 (5109P2) having the same title and filed November 17, 2003) all of which are hereby incorporated by reference in their entirety.

SUMMARY

[0007] In certain embodiments, methods are provided for converting cytosine nucleobases to uracil nucleobases by using a catalyzed bisulfite reaction. In some embodiments, the present invention provides methods for the conversion of cytosine to uracil in a nucleic acid comprising the steps of providing a nucleic acid comprising at least one cytosine nucleobase; and reacting said nucleic acid with bisulfite ion in the presence of a polyamine catalyst.

[0008] In some embodiments, the polyamine catalyst comprises a compound having the Formula I or II:



or a salt or derivative thereof, wherein R_1 , R_2 and R_3 are each independently $-(\text{CH}_2)_n\text{-NH-}]_q\text{-X}$; where n is 1 to 4; q is 0-3; and X is H or C_{1-4} alkyl; provided that at least one q is not 0.

[0009] In some embodiments, the polyamine catalyst comprises is selected from one or more triamines and/or tetraamines. In further embodiments, the polyamine catalyst comprises one or more of diethylene triamine, guanidine, spermine, or their salts and derivatives. In still further embodiments, the polyamine catalyst has the Formula I where R_1 and R_2 are each $-(\text{CH}_2)_2\text{-NH}_2$; and R_3 is H (i.e., diethylene triamine; DETA), guanidine compounds, or other triamine compounds.

[0010] In some embodiments, the reaction of the nucleic acid and bisulfite ion is performed in a solution containing bisulfite ion, preferably in the form of magnesium

bisulfite, in a concentration of from about 0.5M to about 2.5M. In further embodiments, the solution contains bisulfite ion, such as magnesium bisulfite, in a concentration of from about 1M to about 2M.

[0011] In some embodiments, the magnesium bisulfite is present in the reaction mixture at a concentration of at least about 1M.

[0012] Also provided in accordance with the present invention are methods for conversion of cytosine to uracil comprising the steps of reacting a DNA sample in solution with a bisulfite salt and a polyamine catalyst as described above, wherein the concentration of the bisulfite salt is about 0.5M to about 2.5M, and the concentration of the polyamine catalyst is from about 0.06M to about 0.14M. In further embodiments, the final concentration of the bisulfite salt is about 0.8M to about 2M, and the final concentration of the polyamine catalyst is from about 0.06M to about 0.1M.

[0013] In some embodiments of the methods of the invention, the reaction is performed at a temperature of from about 40 to 60 degrees, e.g., about 50 degrees, for about 4 to about 15 hours. In further embodiments of the methods of the invention, the nucleic acid comprises gDNA.

[0014] In some embodiments, the methods of the invention further comprise reacting the bisulfite-treated nucleic acid with a base. In some embodiments, the base is sodium hydroxide (NaOH).

[0015] Also provided in accordance with the present invention are kits for use in conversion of cytosine to uracil comprising a bisulfite such as magnesium bisulfite; and a polyamine catalyst as described above. In some embodiments of such kits, the magnesium bisulfite is provided as an approximately 2M magnesium bisulfite solution. In further embodiments of the kits of the invention, the polyamine catalyst comprises DETA, which in some embodiments is provided as an approximately 2 M DETA solution. In some embodiments, the kits further comprise reagents for sequencing and/or amplification (e.g., by

PCR), for example a polymerase and one or more primers. In some embodiments, the kits contain premeasured materials useful in various embodiments of the methods of the invention.

[0016] In some embodiments, the methylation status of one or more cytosines in the target nucleic acid(s) can be determined by any suitable method. Typically, methylation status can be determined by measuring the presence or relative amount of uracil at a nucleotide position that was previously non-methylated cytosine, and was converted to uracil by the bisulfite treatment. If desired, the presence or relative amount of residual cytosine at the same nucleotide position (indicating the presence of methylcytosine) can be measured for comparison with the amount of uracil, to determine the degree of methylation at the particular nucleotide position. Appropriate control experiments can also be performed to correct for incomplete transformation of cytosine to uracil, if desired.

[0017] The presence or amount of uracil and/or methylcytosine at a particular nucleotide position can be measured by any suitable method, such as DNA sequencing (e.g., by the Sanger method or Maxam-Gilbert method or subsequent embodiments thereof (e.g., using dye-labeled terminators or dye-labeled primers, such as discussed in WO 02/30944 and by Ansorge et al. *DNA Sequencing Strategies – Automated and Advanced Approaches*, John Wiley & Sons, New York, 1997)), PCR (e.g., primer-specific PCR), oligonucleotide ligation assay (OLA) or other ligation-dependent techniques (e.g., see U.S. Patent No. 6,511,810 and references cited therein), single base extension (over the potential methylation site), mass spectrometry, real time PCR (e.g., using labeled probes that are complementary to C and or U), microarrays comprising sequence specific probes, etc. Various exemplary techniques are also described by Kirk et al., *Nucl. Acids Res.*, 30:3295-3311 (2002).

DETAILED DESCRIPTION

[0018] It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the invention, as claimed. In this application, the use of the singular includes the plural unless specifically stated otherwise. In this application, the use of “or” means “and/or” unless stated otherwise. Furthermore, the use of the term “including”, as well as other forms, such as “includes” and “included”, is not intended to be limiting.

[0019] DEFINITIONS

[0020] As used herein, the term “gDNA” refers to genomic DNA.

[0021] Bisulfite ion has its accustomed meaning of HSO_3^- . Typically, bisulfite is used as an aqueous solution of a bisulfite salt, for example magnesium bisulfite, which has the formula $\text{Mg}(\text{HSO}_3)_2$, and sodium bisulfite, which has the formula NaHSO_3 .

[0022] The term “PCR” is intended to denote polymerase chain reaction, as is well known in the art. The term “MSP” denotes methylation specific PCR, such as described by J. Herman, *Proc. Natl. Acad. Sci.* **93**, 9821-26 (1996), and modified as discussed herein.

[0023] As used herein, the term “nucleic acid” includes nucleobase-containing polymeric compounds, including naturally occurring and non-naturally occurring forms thereof, for example and without limitation, genomic DNA, cDNA, hnRNA, mRNA, rRNA, tRNA, fragmented nucleic acids, nucleic acids obtained from subcellular organelles such as mitochondria or chloroplasts, and nucleic acids obtained from microorganisms, or DNA or RNA viruses that may be present on or in a biological sample.

[0024] As used herein, the term “polyamine” is intended to refer to compounds having more than one amine group, and their salts. Thus, “polyamines” include, without limitation, diamines, triamines such as diethylene triamine (DETA), guanidine and tetramethyl guanidine; tetraamines, such as spermine; compounds having the Formula I as disclosed

herein, and other compounds containing two or more amine groups, and salts of the same. In some embodiments, the polyamine has a molecular weight of 1000 or less, or a molecular weight of 500 or less, or a molecular weight of 100 or less.

[0025] The term “quaternary amine compound” is intended to include, without limitation, salts of quaternary ammonium compounds, including without limitation quaternary alkyl ammonium salts. These include, without limitation, quaternary alkyl ammonium halides, for example quaternary methyl ammonium bromide, quaternary ammonium chlorides, tetraethyl ammonium hydroxide, tetraethylammonium chloride, tetrabutyl ammonium chloride, tetrabutyl ammonium bromide, and the like.

[0026] The term “ssDNA” refers to single stranded DNA, resulting typically, but not exclusively, from denaturing double stranded DNA (“dsDNA”).

[0027] The term “TE buffer” refers to the well-known buffering solution of 10mM tris-cl and 1mM EDTA that is typically used in analysis of nucleic acids.

[0028] The term “triamine” refers to compounds having three amino groups, including but not limited to diethylene triamine (DETA), guanidine HCl, tetramethyl guanidine, and the like.

[0029] The term “nucleic acid sample” is intended to denote a sample (e.g., a composition, mixture, suspension or solution) that contains at least one nucleic acid.

Unless otherwise specified, reference herein to cytosine refers to unmethylated cytosine and conversion refers to specific conversion of unmethylated cytosine to uracil.

[0030] In some embodiments, the present invention provides methods of converting cytosine to uracil in a nucleic acid sample by using a catalyzed bisulfite reaction. The methods of the present invention provide significant benefits.

[0031] The nucleic acid samples may be obtained by any conventional collection and purification process prior to use in the methods of the invention. The examples discussed

below used commercially available sample lines (from Coriell or Intergen) of known methylation status, to assess the viability of the methods.

[0032] Typical protocols in the art require the use of freshly made 3M sodium bisulfite, long reaction times of up to 16 hours, and the presence of an antioxidant. Because of the relatively high salt concentration, the low pH of the reaction and the long reaction times, the DNA can be degraded. Additionally, the ss DNA resulting from the gDNA is difficult to purify away from the high concentration of salt used in the reaction. In addition, it is typically necessary to remove most of the bisulfite, which interferes with subsequent enzymatic reactions, for example, those of PCR protocols. Prior procedures also require freshly prepared solutions of bisulfite and antioxidant (typically hydroquinone).

[0033] Embodiments of the present invention may overcome one or more disadvantages of prior methods as briefly described below. For example, it has been discovered in accordance with the some embodiments of the present invention that the reaction of a nucleic acid of interest with bisulfite ion, such as magnesium bisulfite, in the presence of a polyamine catalyst affords faster reaction times. In addition, because the reaction time is faster, less oxidation may occur. Thus, the presently disclosed methods do not require addition of an antioxidant such as hydroquinone. Additionally, magnesium bisulfite solutions (e.g., 1M) may remain acidic in the presence of effective concentrations of polyamine catalyst (for example 0.1M DETA), whereas the corresponding solution of sodium bisulfite salt does not. Thus, methods of the invention can employ bisulfite concentrations that are significantly less than used previously, thereby affording facilitated sample preparation for PCR or other processing. Moreover, it has been discovered herein that stock magnesium bisulfite solutions can be employed, thus eliminating the need to freshly prepare those solutions. Finally, methods of the invention may reduce or eliminate the need for a separate predenaturation step, and can be performed in a greatly reduced reaction volume. Thus, methods of the

present invention can afford PCR yields similar to those of protocols previously known in the art, but with reduced preparation times, reaction times, and clean-up efforts.

[0034] Suitable counter-ions for the bisulfite compound may be monovalent or divalent. Examples of monovalent cations include, without limitation, sodium, lithium, potassium, ammonium, and tetraalkylammonium. Suitable divalent cations include, without limitation, magnesium, manganese, and calcium. A more detailed discussion of uses of quaternary amine catalysts is provided in the application entitled "Method And Materials For Quaternary Amine Catalyzed Bisulfite Conversion Of Cytosine To Uracil" (U.S. application Ser. No. 60/499,106 filed August 29, 2003, and also application Ser. No. 60/_____ (docket no. 5093P2) having the same title and filed concurrently herewith) assigned to the assignee of this application, which is hereby incorporated by reference.

[0035] Typically, the product of the reaction between the nucleic acid and bisulfite is reacted with a base to complete the conversion of cytosine to uracil. One typical base is NaOH. In some embodiments the methods herein further comprise the step of purifying the bisulfite-reacted nucleic acid prior to treatment with base. In some further embodiments, the methods further comprise the step of analyzing the product of the bisulfite conversion reaction, for example by mass spectrometry, to confirm completion of the bisulfite conversion reaction.

[0036] In certain embodiments, the invention comprises kits for carrying out the methods of the invention. In one embodiment, a kit of the invention includes pre-measured ingredients required for carrying out the bisulfite reaction, such as magnesium bisulfite and catalyst. In certain embodiments, the catalyst comprises DETA. In certain embodiments, the invention includes a kit containing pre-packaged materials sufficient to prepare multiple samples. In yet another embodiment, the materials will be pre-packaged with appropriate Eppendorf tubes or other reaction vessels, as appropriate.

[0037] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All documents, or portions of documents, cited in this application, including but not limited to patents, patent applications, articles, books, and treatises, are hereby expressly incorporated by reference in their entirety for any purpose.

[0038] The examples described herein are certain embodiments chosen to illustrate the invention. Applicant does not limit the invention to these embodiments. Rather, Applicant acknowledges that those reasonably skilled in the art will readily recognize additional variants that do not differ from the scope and spirit of the invention.

EXAMPLES

[0039] The Examples below demonstrate the catalytic utility of the illustrative polyamine, diethylene triamine (DETA). DETA was prepared as a 2M solution in accordance with Japanese patent publication JP 1995265082A, which is hereby incorporated by reference. Other polyamines such as the triamine guanidine, derivatives thereof, and the tetra-amine, spermine, were also evaluated, with similar results. Although the use of spermine led to a precipitate, the cytosine to uracil reaction apparently proceeded. The treated nucleic acid product may be further purified if desired, e.g., using an adsorptive technique or dialysis to remove residual reactants.

[0040] Ten samples and one control were prepared with the desired bisulfite reagents and DETA as a catalyst and evaluated on two different plates. Odd numbered samples used the template Univ. Me. methylated DNA, while even numbered samples use the #50 Af. Am. unmethylated DNA template. Sample 11 was a Non Template Control (NTC).

[0041] The samples were treated in accordance with the protocol of J. Herman, *PNAS* **93**, 9821-26 (1996), except as indicated below. This protocol requires the use of a fresh solution

of sodium bisulfite, not more than 30 minutes old, as well as the use of an antioxidant, hydroquinone.

[0042] The magnesium bisulfite used in the Examples described herein was purchased as a 2M $\text{Mg}(\text{HSO}_3)_2$ solution from Aldrich Chemical Co., Milwaukee, Wisconsin. The pH of the purchased solution was 2.6. The solution was used off the shelf, as purchased, and not as a fresh preparation made prior to each use. No antioxidant was used with the magnesium bisulfite. All pH values were measured by pH paper unless otherwise indicated. Sodium bisulfite solutions were made by dissolving solid NaHSO_3 in water.

[0043] Initial attempts to provide easier desalting during the purification portion of the sodium bisulfite reaction protocol by reducing the amount of bisulfite in the reaction led to incomplete conversion. Evaluation of the catalytic effect of the addition of a triamine to the sodium bisulfite reaction showed that the triamine, diethylene triamine, was an effective catalyst. However, it also was surprisingly discovered that an off-the-shelf solution of magnesium bisulfite converted cytosine to uracil similar to reaction with the freshly prepared sodium bisulfite solutions.

[0044] The compositions of Examples 1-10 are shown in Table 1, below:

Table 1

	Examples 1 & 2	Examples 3 & 4	Examples 5 & 6	Examples 7 & 8	Examples 9 & 10
gDNA (diluted to 50 μL with DI water)	1 μg	1 μg	1 μg	1 μg	1 μg
2M NaOH (pre- denaturation step)	5.5 μL	5.5 μL	5.5 μL	5.5 μL	NA

Table 1

	Examples 1 & 2	Examples 3 & 4	Examples 5 & 6	Examples 7 & 8	Examples 9 & 10
10mM Hydro-quinone	30 μ L	30 μ L	30 μ L	30 μ L	NA
Fresh 3.6M NaHSO ₃	520 μ L (to yield 3M)	520 μ L (to yield 3M)	104.5 μ L (to yield 2M)	31.6 μ L (to yield 1M)	NA
2M Mg(HSO ₃) ₂	NA	NA	NA	NA	85.5 μ L To yield approx. 1 M (1.3 M)
2M DETA	NA	5.5 μ L	5.5 μ L	5.5 μ L	5.5 μ L
PH			5.5~6	7	4

[0045] The reaction mixtures in Examples 1-2 were made in strict accordance with the Herman protocol noted above.. The reaction mixtures in Examples 3-8 were made according to the Herman protocol with the addition of DETA and with the shown reduction in volume of sodium bisulfite solution. Examples 9 and 10 were prepared using magnesium bisulfite, as an off-the-shelf commercially available 2M stock solution, rather than a freshly prepared sodium bisulfite solution. In contrast to the Herman protocol, the reaction mixtures in Examples 9 and 10 were not previously denatured, the bisulfite solution was not freshly prepared, no antioxidant was used, the pH was not strictly controlled, and initially, reaction times were just four hours. In later experiments, reactions were allowed to proceed for up to 15 hours. The reaction mixture had a pH of 4. The resultant bisulfite-treated DNA was purified in accordance with the Herman protocol (i.e. using the commercially available DNA Wizard clean-up kit and an EtOH/precipitation step overnight),

[0046] Once the reactions were complete, two separate analyses were conducted to evaluate whether the reaction products were suitable for PCR. First, a "dilute and PCR" approach was used with a small amount of each sample to obtain qualitative results. Second,

for comparison a more complete purification step was conducted using the wizard resin and precipitation as described above..

[0047] Each sample was analyzed by methylation-specific PCR (MSP). MSP provides a relatively fast analysis method for methylation status of bisulfite-treated DNA samples, providing a yes/no answer. The method is based on using primer pair sets. One primer pair is designed to anneal/PCR amplify only if all cytosines were successfully converted to uracil, and the other primer pair in the set annealed/PCR amplified if the methylated cytosine (CpG cytosines only) were methylated, and therefore not converted to uracil.

[0048] The MSP pairs that amplify specific gene fragments, and the expected size of the amplicon, are the following:

[0049] for the *p16* gene, unmethylated reaction (size 151):

[0050] 5'-TTATTAGAGGGTGGGGTGGATTGT-3' (sense),

[0051] 5'-CAACCCCAAACCACAACCATAA-3' (antisense);

[0052] methylated reaction (size 150):

[0053] 5'-TTATTAGAGGGTGGGGCGGATCGC-3' (sense),

[0054] 5'-GACCCCGAACCG-CGACCGTAA-3' (antisense);

[0055] for the *MGMT* gene, unmethylated reaction (93):

[0056] 5'-TTTGTGTTTGTATGTTTGTAGGTTTTTGT-3' (sense),

[0057] 5'-AACTCCACACTCTTCCAAAAACAAAACA-3' (antisense);

[0058] methylated reaction(81):

[0059] 5'-TTTCGACGTTTCGTAGGTTTTTCGC-3' (sense),

[0060] 5'-GCACTCTTCCGAAA-ACGAAACG-3' (antisense);

[0061] for the *DAP-kinase* gene, unmethylated reaction:

[0062] 5'-GGAGGATAGTTGGATTGAGTTAATGTT-3' (sense),

- [0063] 5'- CAATCCCT-CCCAAACACCAA-3' (antisense);
- [0064] methylated reaction:
- [0065] 5'-GGATAGTCGGATCGAGTTAACGTC-3' (sense),
- [0066] 5'-CCCTCCCAAACGCCG-3' (antisense);
- [0067] for the *MLH1* gene, unmethylated reaction (124):
- [0068] 5'- TTTTGATGTAGATGTTTTATTAGGGTTGT (sense)
- [0069] 5'- ACCACCTCATCATAACTACCCACA (antisense)
- [0070] methylated reaction (115)
- [0071] 5'- ACGTAGACGTTTTATTAGGGTCGC (sense)
- [0072] 5'- CCTCATCGTAACTACCCGCG (antisense)
- [0073] for the *p15* gene, unmethylated reaction (154):
- [0074] 5'-TGTGATGTGTTTGTATTTTGTGGTT (sense)
- [0075] 5'-CCATACAATAACCAAACAACCAA (antisense)
- [0076] methylated reaction (148)
- [0077] 5'-GCGTTCGTATTTTGCGGTT (sense)
- [0078] 5'-CGTACAATAACCGAACGACCGA (antisense)
- [0079] The PCR recipe used to evaluate the samples was:

2X Taq Gold PCR Master Mix	10 μ L
Fwd primer (5 uM)	1 μ L
Rev primer (5uM)	1 μ L
Bisulfite treated DNA	0.5 μ L
H2O	7.5 μ L

	20 μ L

[0080] 2X TaqGold PCR master mix is commercially available from Applied Biosystems. The forward and reverse primer sequences are those listed above.

[0081] The following thermal cycling schedule was used:

	95 deg 5 min
40 cycles	95 deg 30sec
	60 deg 45 sec
	72 deg 1:00 min
	4 deg forever

[0082] One of the primers in each set was synthesized with a 5'FAM label. A 1 uL aliquot of the above PCR reaction was added to HiDi formamide with ROX 500 size standard added, and denatured by heating at 95°C for 5 min. By using a FAM-labeled primer, the PCR amplicon was directly analyzed on an ABI PRISM® 310 Genetic Analyzer, with POP-4™ polymer, using run module “GS POP4 (1mL) A” (reagents and instrument all from Applied Biosystems).

[0083] The presence of a PCR amplicon (i.e. a “peak”) having the correct size as observed using the 310 Genetic Analyzer indicated a successful reaction. Additionally, the height or area of the peak could be used empirically to determine how much template (i.e. bisulfite-treated gDNA) was initially present. The bigger the peak, the more DNA was initially present.

[0084] If bisulfite-conversion is incomplete, MSP can sometimes give a “false positive” or an overestimate in the amount of cytosine methylation due to the counting of unreacted cytosine nucleobases as methyl-cytosine nucleobases (see e.g. Table 2, p16U, sample 3, below). Accordingly, control reactions can be performed to establish conditions that afford substantially quantitative conversion of cytosine to uracil nucleobases. Alternatively, control reactions can be performed to measure the efficiency of the conversion, to allow subtraction

of unreacted, non-methylated cytosine nucleobases from experimental results so that the amount of methylation can be determined more accurately. For example, synthetic DNA containing non-methylated cytosine can be used to assess the conversion yield to uracil following bisulfite treatment. For example, an 80% yield obtained with synthetic DNA would indicate that correction factor of 20% should be applied (subtracted) from the amount of methylated cytosine that is observed experimentally for a sample of interest.

[0085] The results in Table 2 show that the efficiency of the conversion reaction of cytosine to uracil nucleobases was improved by the addition of the polyamine catalyst, DETA. PCR yields in all cases were similar to or greater than those obtained with the uncatalyzed 3M sodium bisulfite treated sample lacking polyamine catalyst. Furthermore, the results indicate that 2M sodium bisulfite with catalyst produces yields similar to, or better than, the catalyzed 3M sodium bisulfite yields. Poorer results were obtained using 1M sodium bisulfite, even with catalyst.

[0086] The Applicant(s) have discovered that good conversion yields can be obtained using $\text{Mg}(\text{HSO}_3)_2$ (e.g., 1 M concentration), optionally with a polyamine catalyst, and without addition of hydroquinone or other antioxidant. For example, PCR yields with $\text{Mg}(\text{HSO}_3)_2$ have been found to be at least comparable or superior to yields obtained using sodium bisulfite yields at concentrations of 2 to 3 M

[0087] This finding is surprising and unexpected, particularly in view of the fact that the magnesium bisulfite solution need not be made fresh, as is usually required for the sodium bisulfite solution. Initially, it was possible that the off-the-shelf magnesium bisulfite solution would suffer from degradation to SO_2 , which would account for the low pH seen initially. Accordingly, it was predicted that the magnesium bisulfite treated samples would not achieve effective PCR yields. However, the data in Table 2 demonstrates results quite to the contrary.

TABLE 2

	1	2	3	4	5	6	7	8	9	10	NTC Ctrl 11
p16 M	X	X	1200	X	1600	X	X	X	<i>X*</i>	X	X
p16 U	<i>Small peak</i>	4500	<i>5600</i>	X	5600	X	X	X	X	4000	<i>4000</i>
mgmt M	6000	X	6000	X	6000	X	X	X	6000	X	X
mgmt U	X	1600	X	2000	X	2000	X	X	X	5000	X
mlh 1 M	2000	X	2000	X	2000	X	X	X	2000	X	X
mlh 1 U	X	1600	X	1600	X	1600	X	X	X	2000	X
er M	2400	X	2400	X	2400	X	X	X	2400	X	X
er U	X	Very small	X	1600	X	1600	X	X	X	1400	X
p14 M	~400	X	2000	X	2000	<i>2000 *</i>	6000	<i>6000</i>	6000	X	X
p14 U	X	3000	X	3000	X	7000	X	X	X	6000	X
gstp M	300	X	500	X	300	X	X	X	200	X	X
gstp U	X	5000	X	5000	X	5000	X	X	X	2000	X
dapk M	2000	X	2000	X	2000	<i>2000</i>	X	X	2000	X	X
dapk U	X	3000	X	5000	X	7000	X	X	X	3200	X
p15 M	2000	X	2000	X	2000	X	X	X	3200	X	X
p15 U	X	400	X	200	X	800	X	X	X	1600	X

* *Bold italics* indicates unexpected result

[0088] The MSP-PCR product was then sometimes sequenced for further "resolution". DNA sequencing was performed using standard protocols and reagents from Applied Biosystems.

[0089] Prior to sequencing of the PCR amplicon, the primers and excess dNTPs used during the MSP-PCR were removed by treatment of a 4 μ L aliquot of the PCR reaction with an equal volume mixture containing 2 Units each of Shrimp Alkaline Phosphatase (SAP) and exonuclease 1 (exo) (USB Corporation, Cleveland, OH). The reaction was incubated at 37°C for 1 hr, and then heat-denatured at 75°C for 15 min. A 4 μ L aliquot of the exo/SAP reaction was added to a solution containing 1-4 μ L of BigDye® Terminator v1.1 cycle sequencing reaction mix (Applied Biosystems), 2 μ L of BigDye® Terminator v1.1 5X sequencing buffer, 2 μ L of the reverse PCR primer (5 uM)(which did not have a FAM-label), and enough water for a final volume of 20 μ L. Thermal cycling: 95°C/1min, 50 cycles of 96°C/10sec, 52°C/10sec, 60°C/4 min, and stored at 4°C. The cycle-sequencing reaction products were purified by an Edge Biosystems Performa® 96-well plate, dried under vacuum, dissolved in 12 μ L of HiDi Formamide and analyzed on an ABI Prism 3730 DNA Analyzer with KB basecaller or a 3700 DNA Analyzer.

[0090] DNA sequencing permitted evaluation of each cytosine in the gene region that was amplified by the MSP primer sets, allowing assessment of the degree of cytosine to uracil conversion.

[0091] The studies herein utilized 2M magnesium bisulfite stock solutions, which were diluted with the sample to produce a final magnesium bisulfite concentration of about 1M. Use of a more concentrated magnesium bisulfite solution would yield higher bisulfite concentration for conversion, while still keeping reaction volumes to a minimum. Such increased bisulfite concentration in the reaction mixture could easily be employed, and would be expected to enhance bisulfite conversion of cytosine to uracil. The optimization of such

reaction parameters, including volume and/or concentration of magnesium bisulfite solution, temperature, pH and other reaction conditions are expected to lead to more complete conversion, and are well within the skill of the art.

[0092] To verify that the magnesium bisulfite reaction is specific for cytosine but not methyl cytosine, a model system was created. A synthetic, four base oligonucleotide, ATCG, was employed to determine the rate of conversion by HPLC. On a ds Eclipse HP column, using 0.1M TEAA = A and 0.1M TEAA with 25% CH₃CN = B. ATCG and AT^{Me}CG were treated in accordance with the catalyzed magnesium bisulfite reaction described above and directly analyzed by HPLC to evaluate the specificity of the reaction. The results indicated that after 22 minutes, at 50°C, the catalyzed 1M magnesium bisulfite treated ATCG reacted to yield ATUG. Under the same reactions conditions, the AT^{Me}CG did not react. Thus, these results indicate that the catalyzed magnesium bisulfite reaction is specific for the conversion of unmethylated cytosine to uracil. Accordingly, utilization of magnesium bisulfite can have great utility in methylation assessment.

[0093] Further tests performed with 0.06-0.1M DETA provided similar results. The pH reached 5-7 when 0.2, 0.26, and 0.33M DETA was used. In the 0.26 and 0.33M samples, a precipitate was formed, but it was not detrimental to the reactions.

[0094] In addition to DETA, the guanidine based triamines guanidine HCl (0.27M-0.6M) and tetramethylguanidine (0.2M) also were used. The guanidine compounds are denaturants to help maintain single stranded DNA during bisulfite conversion. The model HPLC system is not useful in studying the effect of denaturation.

[0095] In some further experiments, the denaturant TBAC or TBAB, alone, and in combination with DETA were employed. For example, bisulfite conversion of gDNA was carried out successfully using a mixture of TBAC and DETA.

[0096] It also was observed using HPLC that NaOH added to the magnesium bisulfite reaction increased the rate of reaction of the oligonucleotide ATCG, due to the raised pH.

The results presented herein also show that magnesium bisulfite, even without catalyst, converts cytosine to uracil. The preferred pH range of this conversion reaction is about 2.6-4.0. Raising pH beyond this range typically results in an undesirable precipitate.

[0097] Also useful is a new clean-up procedure, employing size exclusion, which appears to improve product yields, as described in a separate patent application by the present inventors entitled "Improved Bisulfite Method" (U.S. application Ser. No. 60/498,996 filed August 29, 2003, and also application Ser. No. 60/520,941 (5109P2) (having the same title and filed November 17, 2003) hereby incorporated by reference in their entirety. The process uses a Microcon 100 (Millipore), or similar, size-exclusion device. According to one embodiment of that method, the sample and 200 μ L of water was added to the Microcon 100 device, and the sample was then spun in the device at approximately 2800 RPM for about 8 minutes (as per manufacturers recommendation). The resultant filtrate was removed. Two subsequent washes with about 300 μ L water, each spun at about 2800 RPM for 8 minutes followed. After each, the filtrate was again removed. About 300 μ L 0.1N NaOH was added and spun at approximately 2800 RPM for about 8 minutes. Again, the filtrate was removed. After addition of about 300 μ L of water, the sample was spun in the device at 2800 RPM for about 6-8 minutes. The filtrate was removed and about 50 μ L TE buffer (approximately pH 8) was added. After about 5 minutes before it was inverted to collect the purified DNA sample in a centrifuge. Approximately 60 μ L were collected.

[0098] Although the antioxidant, hydroquinone, is not required in the magnesium bisulfite reactions, and in light of these findings may not be needed in the sodium bisulfite reactions, it can be used without negative effect in the methods of the invention.

[0099] The inventors are not limited to these embodiments or any of the examples above described herein, but rather acknowledge that other variants of these methods will be

apparent to those skilled in the art and are within the scope and spirit of the invention disclosed herein.

[00100] Other variants of the catalyzed bisulfite reactions described herein will be apparent to those of reasonable skill in the art and area considered within the scope and spirit of the invention and disclosed and claimed herein.

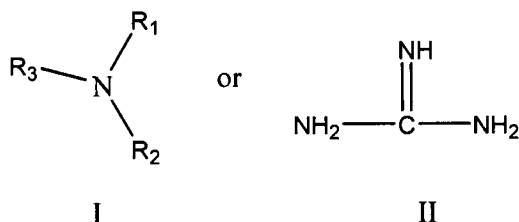
CLAIMS

What is claimed is:

1. A method for converting cytosine to uracil comprising the steps of:

providing a nucleic acid comprising at least one cytosine nucleobase; and

reacting said nucleic with bisulfite ion in the presence of a polyamine catalyst.
2. The method of claim 1 wherein said reacting is performed in the presence of a polyamine catalyst having the Formula I or II:



or a salt or derivative thereof, wherein:

R_1 , R_2 and R_3 re each independently $-\text{[(CH}_2\text{)}_n\text{-NH-]}_q\text{-X}$;

n is 1 to 4;

q is 0-3; and

X is H or C_{1-4} alkyl; provided that at least one q is not 0.

3. The method of claim 1 wherein said polyamine catalyst comprises at least one of a triamine and/or a tetraamine.
4. The method of claim 1 wherein said catalyst comprises a triamine selected from at least one of a diethylene triamine, a guanidine, and a salt or derivative thereof.

5. The method of claim 2 wherein said reaction is performed in the presence of a catalyst having Formula I, wherein R_1 and R_2 are each $-(CH_2)_2-NH_2$; and R_3 is H.
6. The method of claim 2 wherein said catalyst comprises guanidine.
7. The method of claim 2 wherein said catalyst comprises spermine.
8. The method of claim 1 wherein said reacting is performed in a solution containing bisulfite ion having a concentration of from about 0.5M to about 2.5M.
9. The method of claim 8 wherein said solution contains bisulfite ion having a concentration of about 1M to about 2M.
10. The method of claim 1 wherein said reacting is performed in a solution comprising magnesium bisulfite having a concentration of from about 0.5M to about 2.5M.
11. The method of claim 10 wherein said solution comprises magnesium bisulfite having a concentration of from about 1M to about 2M.
12. The method of claim 2 wherein said reacting is performed in a solution comprising magnesium bisulfite having a concentration of from about 0.5M to about 2.5M.
13. The method of claim 5 wherein said reacting is performed in a solution comprising magnesium bisulfite having a concentration of from about 0.5M to about 2.5M.
14. The method of claim 6 wherein said reacting is performed in a solution comprising magnesium bisulfite having a concentration of from about 0.5M to about 2.5M.
15. The method of claim 1 wherein said reacting is performed in the presence of magnesium bisulfite having a concentration of at least about 1M.

16. A method for converting a cytosine nucleobase to a uracil nucleobase comprising the steps of:

reacting a DNA sample in solution with a bisulfite salt and a polyamine catalyst, wherein the final concentration of said bisulfite is about 0.5M to about 2.5M, and the final concentration of said polyamine catalyst is from about 0.06M to about 0.14M.

17. The method of claim 16 wherein said final concentration of said bisulfite is about 0.8M to about 1.2M, and the final concentration of said polyamine catalyst is from about 0.06M to about 0.1M.

18. The method of claim 16 wherein said reaction is performed at a temperature of from about 40 degrees to about 60 degrees for about 4 to about 15 hours.

19. The method of claim 16 wherein said bisulfite salt is magnesium bisulfite, and said polyamine catalyst is diethylene triamine.

20. The method of claim 19 wherein said reaction is performed at about 50 degrees for about 4 to about 15 hours.

21. The method of claim 1 wherein said nucleic acid is gDNA.

22. The method of claim 1 further comprising treating the product of said reaction of said nucleic acid and said bisulfite ion with a base.

23. The method of claim 22 wherein said base comprises NaOH.

24. A kit for use in conversion of cytosine to uracil comprising:
magnesium bisulfite; and
a polyamine catalyst.

25. The kit of claim 24, wherein said magnesium bisulfite is provided as an approximately 2M magnesium bisulfite solution.

26. The kit of claim 24, wherein said polyamine catalyst comprises DETA.

27. The kit of claim 26, wherein said DETA is provided as an approximately 2 M DETA solution.

28. The kit of claim 24 further comprising a nucleotide polymerase and one or more primers for sequencing or amplification.